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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: MINETTI, CONCEICAO;
MICHON, FRANCIS;
PULLEN, JEFFREY K.;
POLDVINO-BODNAR, MARYELLEN;
LIANG, SHU-MEI;
TAI, JOSEPH Y.
- (ii) TITLE OF INVENTION: MODIFIED IMMUNOGENIC
PNEUMOLYSIN COMPOSITIONS AS VACCINES
- (iii) NUMBER OF SEQUENCES: 18
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
 - (B) STREET: 345 PARK AVENUE
 - (C) CITY: NEW YORK
 - (D) STATE: NEW YORK
 - (E) COUNTRY: USA
 - (F) ZIP: 10154
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: FLOPPY DISK
 - (B) COMPUTER: IBM PC COMPATIBLE
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: MICROSOFT WORD 97
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/120,044
 - (B) FILING DATE: 1998-07-21
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 60/053,306
 - (B) FILING DATE: 1997-07-21
- (viii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 60/073,456
 - (B) FILING DATE: 1998-02-02
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: DARRYL H. STEENSMA
 - (B) REGISTRATION NUMBER: 43,155

(C) REFERENCE/DOCKET NUMBER: 1758-4036US2

- (ix) TELECOMMUNICATION INFORMATION:
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(C) TELEX: 421792

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1413
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *S. pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

atggcaaata aagcagtaaa tgactttata ctagctatga	40
attacgataa aaagaaactc ttgacccatc agggagaaag	80
tattgaaaat cgtttcatca aagagggtaa tcagctaccc	120
gatgagtttg ttgttatcga aagaaagaag cggagcttgt	160
cgacaaatac aagtgatatt tctgtaacag ctaccaacga	200
cagtcgcctc tatcctggag cacttctcgt agtggatgag	240
accttgttag agaataatcc cactcttctt gcggtcgatc	280
gtgctccgat gacttatagt attgatttgc ctggtttggc	320
aagtagcgat agctttctcc aagtggaaga tcccagcaat	360
tcaagtgttc gcggagcggg aaacgatttg ttggctaagt	400
ggcatcaaga ttatggtcag gtcaataatg tcccagctag	440
aatgcagtat gaaaaaatca cggctcacag catggaacaa	480

ctcaaggtca agtttggttc tgactttgaa aagacagggga	520
attctcttga tattgatttt aactctgtcc attcaggcga	560
aaagcagatt cagattgtta attttaagca gatttattat	600
acagtcagcg tagacgctgt taaaaatcca ggagatgtgt	640
ttcaagatac tgtaacggta gaggatttaa aacagagagg	680
aatttctgca gagcgtcctt tggctctatat ttcgagtgtt	720
gcttatgggc gccaaagtcta tctcaagttg gaaaccacga	760
gtaagagtga tgaagtagag gctgcttttg aagctttgat	800
aaaaggagtc aaggtagctc ctcagacaga gtggaagcag	840
attttggaca atacagaagt gaaggcgggtt attttagggg	880
gcgacccaag ttcgggtgcc cgagttgtaa caggcaaggt	920
ggatatggta gaggacttga ttcaagaagg cagtcgcttt	960
acagcagatc atccaggctt gccgatttcc tatacaactt	1000
cttttttacg tgacaatgta gttgcgacct ttcaaaatag	1040
tacagactat gttgagacta aggttacagc ttacagaaac	1080
ggagatttac tgctggatca tagtggtgcc tatgttgccc	1120
aatattatat tacttggaat gaattatcct atgatcatca	1160
aggtaaggaa gtcttgactc ctaaggcttg ggacagaaat	1200
gggcaggatt taacggctca ctttaccact agtattcctt	1240
taaaagggaa tgttcgtaat ctctctgtca aaattagaga	1280
gtgtaccggg cttgcttggg aatggtggcg tacggtttat	1320
gaaaaaaccg atttgccact agtgcgtaag cggacgattt	1360
ctatttgggg aacaactctc tatccgcagg tagaagataa	1400

ggtagaaaat gac

1413

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1413
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *S. pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

atggcaaata aagcagtaaa tgactttata ctagctatga	40
attacgatan aaanaaactc ttgacccatc agggagaaag	80
tattgaaaat cgtttcanca aagagggtaa tcagctaccc	120
gntgagtttg ttgntancga aagaaagaag cggagcttgt	160
cgacaaatac aagtgatatt nctgtancag ctaccnacga	200
cagtcgcctc tatectggag cacttctcgt agtggatgag	240
accttgtnag agaataatcc cactcttctt gcggtngatc	280
gtgctccgat gacttatagt antgntttgc ctggtttggc	320
aagtagcgat agctttctcc aagtggaaga ncccagcaat	360
tcaagtgttc gcggagcggn anacgatttg ttggctaagt	400
ggcatcaaga ttatggtcag gtcaataatg tcccagctag	440
aangcagtat gaaaaaatna cggctcacag catggaacaa	480
ctcaagggtca agtttggttc tgactttgaa aagncaggga	520
attctcttga tattgatttt aactctgtcc attcaggnga	560

aaagcngatt cagattgtta atnttaagca gatttattat	600
acagtcagcg tagacgctgt taaaaatcca ggagatgtgt	640
ttcaagatac tgtaacggta gaggatttaa aacagagagg	680
aattttctgca gagcgtcctt tggctctatat ttcgagngtt	720
gcttatgggc gccaaagtcta tctcaagttg gaaaccacga	760
gtangagtgn tgaagtagag gctgcttttg aagctttgat	800
aaaaggagtc aaggtagctc ctcagacaga gtggaagcag	840
attttggaaca atacagaagt gaaggcgggtt attttagggg	880
gcgacccaag ttcgggtgcc cgagttgtaa caggcaaggt	920
ggatatggta gaggacttga ttcaagaagg cagtcgcttt	960
acagcagatc atccaggctt gccgatttcc tatacaactt	1000
cttttttacg tgacaatgta gttgcgacct ttcaaaanag	1040
tacagactat gttgagacta aggttacagc ttacagaaac	1080
ggagatttac tgctggatca tagtggtgcc tatgttgccc	1120
aatattatat tacttggnat gaattatcct atgatcatca	1160
aggtaaggaa gtcttgactc ctaaggcttg ggacagaaat	1200
gggcaggatt tnacggctca ctttaccact agtattcctt	1240
taaaagggaa tgttcgtaat ctctctgtca aaattagaga	1280
gtgtaccggg cttgcntggg aatgggtggcg tacggtttat	1320
gaaaaaaccg atttgccact agtgcgtaag cggacgattt	1360
ctatttgggg aacaactctc tatecncagg tagangataa	1400
ggtagaaaat gac	1413

Met	Ala	Asn	Lys	Ala	Val	Asn	Asp	Phe	Ile	Leu	Ala	
1				5					10			
Met	Asn	Tyr	Asp	Lys	Lys	Lys	Leu	Leu	Thr	His	Gln	
		15					20					
Gly	Glu	Ser	Ile	Glu	Asn	Arg	Phe	Ile	Lys	Glu	Gly	
25					30					35		
Asn	Gln	Leu	Pro	Asp	Glu	Phe	Val	Val	Ile	Glu	Arg	
			40					45				
Lys	Lys	Arg	Ser	Leu	Ser	Thr	Asn	Thr	Ser	Asp	Ile	
	50					55					60	
Ser	Val	Thr	Ala	Thr	Asn	Asp	Ser	Arg	Leu	Tyr	Pro	
				65					70			
Gly	Ala	Leu	Leu	Val	Val	Asp	Glu	Thr	Leu	Leu	Glu	
		75					80					
Asn	Asn	Pro	Thr	Leu	Leu	Ala	Val	Asp	Arg	Ala	Pro	
85					90					95		
Met	Thr	Tyr	Ser	Ile	Asp	Leu	Pro	Gly	Leu	Ala	Ser	
		100						105				
Ser	Asp	Ser	Phe	Leu	Gln	Val	Glu	Asp	Pro	Ser	Asn	
	110				115						120	
Ser	Ser	Val	Arg	Gly	Ala	Val	Asn	Asp	Leu	Leu	Ala	
				125					130			
Lys	Trp	His	Gln	Asp	Tyr	Gly	Gln	Val	Asn	Asn	Val	
	135						140					
Pro	Ala	Arg	Met	Gln	Tyr	Glu	Lys	Ile	Thr	Ala	His	
145					150					155		
Ser	Met	Glu	Gln	Leu	Lys	Val	Lys	Phe	Gly	Ser	Asp	
			160					165				

Phe	Glu	Lys	Thr	Gly	Asn	Ser	Leu	Asp	Ile	Asp	Phe
170						175					180
Asn	Ser	Val	His	Ser	Gly	Glu	Lys	Gln	Ile	Gln	Ile
				185						190	
Val	Asn	Phe	Lys	Gln	Ile	Tyr	Tyr	Thr	Val	Ser	Val
	195					200					
Asp	Ala	Val	Lys	Asn	Pro	Gly	Asp	Val	Phe	Gln	Asp
205					210					215	
Thr	Val	Thr	Val	Glu	Asp	Leu	Lys	Gln	Arg	Gly	Ile
			220					225			
Ser	Ala	Glu	Arg	Pro	Leu	Val	Tyr	Ile	Ser	Ser	Val
230						235					240
Ala	Tyr	Gly	Arg	Gln	Val	Tyr	Leu	Lys	Leu	Glu	Thr
				245					250		
Thr	Ser	Lys	Ser	Asp	Glu	Val	Glu	Ala	Ala	Phe	Glu
		255					260				
Ala	Leu	Ile	Lys	Gly	Val	Lys	Val	Ala	Pro	Gln	Thr
265					270					275	
Glu	Trp	Lys	Gln	Ile	Leu	Asp	Asn	Thr	Glu	Val	Lys
			280					285			
Ala	Val	Ile	Leu	Gly	Gly	Asp	Pro	Ser	Ser	Gly	Ala
290						295					300
Arg	Val	Val	Thr	Gly	Lys	Val	Asp	Met	Val	Glu	Asp
				305					310		
Leu	Ile	Gln	Glu	Gly	Ser	Arg	Phe	Thr	Ala	Asp	His
		315					320				
Pro	Gly	Leu	Pro	Ile	Ser	Tyr	Thr	Thr	Ser	Phe	Leu
325					330					335	
Arg	Asp	Asn	Val	Val	Ala	Thr	Phe	Gln	Asn	Ser	Thr
			340					345			
Asp	Tyr	Val	Glu	Thr	Lys	Val	Thr	Ala	Tyr	Arg	Asn
350						355					360
Gly	Asp	Leu	Leu	Leu	Asp	His	Ser	Gly	Ala	Tyr	Val
				365					370		
Ala	Gln	Tyr	Tyr	Ile	Thr	Trp	Asn	Glu	Leu	Ser	Tyr
		375					380				
Asp	His	Gln	Gly	Lys	Glu	Val	Leu	Thr	Pro	Lys	Ala
385					390					395	
Trp	Asp	Arg	Asn	Gly	Gln	Asp	Leu	Thr	Ala	His	Phe
			400					405			
Thr	Thr	Ser	Ile	Pro	Leu	Lys	Gly	Asn	Val	Arg	Asn
410						415					420
Leu	Ser	Val	Lys	Ile	Arg	Glu	Cys	Thr	Gly	Leu	Ala
				425					430		
Trp	Glu	Trp	Trp	Arg	Thr	Val	Tyr	Glu	Lys	Thr	Asp
		435					440				

Leu Pro Leu Val Arg Lys Arg Thr Ile Ser Ile Trp
 445 450 455
 Gly Thr Thr Leu Tyr Pro Gln Val Glu Asp Lys Val
 460 465
 Glu Asn Asp
 470

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *S. pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Asn Lys Ala Val Asn Asp Phe Ile Leu Ala
 1 5 10
 Met Asn Tyr Asp Xaa Xaa Lys Leu Leu Thr His Gln
 15 20
 Gly Glu Ser Ile Glu Asn Arg Phe Xaa Lys Glu Gly
 25 30 35
 Asn Gln Leu Pro Xaa Glu Phe Val Xaa Xaa Glu Arg
 40 45
 Lys Lys Arg Ser Leu Ser Thr Asn Thr Ser Asp Ile
 50 55 60
 Xaa Val Xaa Ala Thr Xaa Asp Ser Arg Leu Tyr Pro
 65 70
 Gly Ala Leu Leu Val Val Asp Glu Thr Xaa Leu Glu
 75 80
 Asn Asn Pro Thr Leu Leu Ala Val Asp Arg Ala Pro
 85 90 95
 Met Thr Tyr Ser Xaa Xaa Leu Pro Gly Leu Ala Ser
 100 105
 Ser Asp Ser Phe Leu Gln Val Glu Asp Pro Ser Asn
 110 115 120
 Ser Ser Val Arg Gly Ala Xaa Xaa Asp Leu Leu Ala
 125 130
 Lys Trp His Gln Asp Tyr Gly Gln Val Asn Asn Val
 135 140

Pro	Ala	Arg	Xaa	Gln	Tyr	Glu	Lys	Xaa	Thr	Ala	His		
145						150					155		
Ser	Met	Glu	Gln	Leu	Lys	Val	Lys	Phe	Gly	Ser	Asp		
			160					165					
Phe	Glu	Lys	Xaa	Gly	Asn	Ser	Leu	Asp	Ile	Asp	Phe		
170						175					180		
Asn	Ser	Val	His	Ser	Gly	Glu	Lys	Xaa	Ile	Gln	Ile		
			185						190				
Val	Asn	Xaa	Lys	Gln	Ile	Tyr	Tyr	Thr	Val	Ser	Val		
		195				200							
Asp	Ala	Val	Lys	Asn	Pro	Gly	Asp	Val	Phe	Gln	Asp		
205					210					215			
Thr	Val	Thr	Val	Glu	Asp	Leu	Lys	Gln	Arg	Gly	Ile		
			220					225					
Ser	Ala	Glu	Arg	Pro	Leu	Val	Tyr	Ile	Ser	Xaa	Val		
230						235					240		
Ala	Tyr	Xaa	Arg	Gln	Val	Tyr	Leu	Lys	Leu	Glu	Thr		
			245						250				
Thr	Ser	Xaa	Ser	Xaa	Glu	Val	Glu	Ala	Ala	Phe	Glu		
		255					260						
Ala	Leu	Ile	Lys	Gly	Val	Lys	Val	Ala	Pro	Gln	Thr		
265					270					275			
Glu	Trp	Lys	Gln	Ile	Leu	Asp	Asn	Thr	Xaa	Val	Lys		
			280					285					
Ala	Val	Ile	Leu	Gly	Gly	Asp	Pro	Ser	Ser	Gly	Ala		
290						295					300		
Arg	Val	Val	Thr	Gly	Lys	Val	Asp	Met	Val	Glu	Asp		
			305						310				
Leu	Ile	Gln	Glu	Gly	Ser	Arg	Phe	Thr	Ala	Asp	His		
		315					320						
Pro	Gly	Leu	Pro	Ile	Ser	Tyr	Thr	Thr	Ser	Phe	Leu		
325					330					335			
Arg	Asp	Asn	Val	Val	Ala	Thr	Phe	Gln	Asn	Ser	Thr		
			340					345					
Asp	Tyr	Val	Glu	Thr	Lys	Val	Thr	Ala	Tyr	Arg	Asn		
350						355					360		
Gly	Asp	Leu	Leu	Leu	Asp	His	Ser	Gly	Ala	Tyr	Val		
			365						370				
Ala	Gln	Tyr	Tyr	Ile	Thr	Trp	Xaa	Glu	Leu	Ser	Tyr		
		375					380						
Asp	His	Gln	Gly	Lys	Glu	Val	Leu	Thr	Pro	Lys	Ala		
385					390					395			
Trp	Asp	Arg	Asn	Gly	Gln	Asp	Leu	Thr	Ala	His	Phe		
			400					405					
Thr	Thr	Ser	Ile	Pro	Leu	Lys	Gly	Asn	Val	Arg	Asn		
410						415					420		

Leu	Ser	Val	Lys	Ile	Arg	Glu	Cys	Thr	Gly	Leu	Ala
				425					430		
Trp	Glu	Trp	Trp	Arg	Thr	Val	Tyr	Glu	Lys	Thr	Asp
		435					440				
Leu	Xaa	Leu	Val	Arg	Lys	Arg	Thr	Ile	Ser	Ile	Trp
445					450					455	
Gly	Thr	Thr	Leu	Tyr	Pro	Gln	Val	Glu	Asp	Lys	Val
			460						465		
Glu	Asn	Asp									
	470										

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *S. pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

aaccttgatt gatctagata aggtatttat gttgg

35

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *S. pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

tctttttgtc tctagaattc tcctctccta gtc

33

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *S. pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

tattaggagg agcatatggc aaataaagca gtaaattg

37

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *S. pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ggcctctttt tgtctcgagc attctcctct cctagtc

37

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *S. pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

attacgcgac tcactatagg g

21

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *S. pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

attacgaaca ttccctttag g

21

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *S. pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ggtcagggtca ataatgtccc agctagaaag cagtatg

37

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *S. pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

gctgtgagcc gtgatttttt catactgctt tctagctg

38

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *S. pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

gcagattcag attgttaatg ttaagcagat ttattata

38

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *S. pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

atctgcttaa cattaacaat ctgaatctgc ttttcgcc

38

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *S. pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

cagattgtta atattaagca gatttattat acagtcagc

39

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *S. pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

aatctgctta atattaacaa tctgaatctg cttttcgcc

39

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *S. pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

acaagtgata ttctgtaac agctaccaac gacagtcgc

39

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *S. pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

agctgttaca ggaatatcac ttgtatttgc cgacaagct

39